Amendments to the Specification:

Please amend the paragraph beginning at line 23 of page 12 with the following amended paragraph:

Nucleic acid arrays that are useful in the present invention include those that are commercially available from Affymetrix (Santa Clara, CA) under the brand name GENECHIP® ~~GeneChip®~~. Example arrays are shown on the website at affymetrix.com.

Please amend the paragraph beginning at line 17 of page 21 with the following amended paragraph:

Preferred arrays are commercially available from Affymetrix under the brand name GENECHIP® ~~GeneChip®~~ and are directed to a variety of purposes, including genotyping and gene expression monitoring for a variety of eukaryotic and prokaryotic species. (*See* Affymetrix Inc., Santa Clara and their website at affymetrix.com.)

Please amend the paragraph beginning at line 21 of page 49 with the following amended paragraph:

Nine human breast cancer cell lines (BT-20, MCF-7, MCF-12A, MDA-MB-157, MDA-MB-436, MDA-MB-468, SK-BR-3, ZR-75-1, and ZR-75-30) and two syngeneic human breast cancer cell lines (Hs-578T and Hs-578Bst) (Hackett et al. (1977) *J Natl Cancer Inst,* Vol. 58, pp.1795-806) were obtained from American Type Culture Collection (ATCC). A normal human mammary epithelial cell line (HMEC) was obtained from Clonetics. All cells were grown under recommended culture conditions. Genomic DNA was isolated using QIAGEN QIAAMP™ ~~QIAamp~~ DNA Blood Mini Kit. DNAs from cell lines containing 3X (NA04626), 4X (NA01416), and 5X (NA06061) chromosomes and DNAs for the normal reference set of 110

individuals (48 males and 62 females) were purchased from NIGMS Human Genetic Cell Repository, Coriell Institute for Medical Research (Camden, NJ).

Please amend the paragraph beginning at line 9 of page 50 with the following amended paragraph:

The WGSA assay was performed as described in Kennedy et al. (2003) except for modifications to the target amplification and DNA labeling steps. DNA amplification by PCR was done under following conditions: each 100 µl reaction contained 25 ng of adaptor-ligated genomic DNA, 0.75 µM primer, 250 µM dNTPs, 2.5 mM $MgCl_2$, 10 U AMPLITAQ GOLD™ polymerase ~~AmpliTaq Gold~~ (Applied Biosystems (ABI)) in 1X PCR Buffer II (ABI). Cycling was performed as follows: 95°C/3 min, followed with 35 cycles of 95°C/30 sec, 59°C/30 sec, 72°C/30 sec, and an extension at 72°C for 7 min. The PCR products were purified and concentrated with QIAGEN MinElute PCR Purification kit and DNA concentrations were measured by A 260 nm. Fragmented DNA was labeled in l 1X TdT buffer with 105 U TdT (Promega) and 0.1429 mM DLR (Affymetrix) at 37°C for 2 hrs, followed by heat inactivation at 95°C for 15 min. DNA hybridization to the AFFYMETRIX GENECHIP® ~~Affymetrix® Gene Chip®~~ 10K Mapping Xba_131 Array, washing, staining, and scanning were performed as specified in the manufacturer's instructions (Affymetrix). All samples except the normal reference set were tested in duplicate. The call rates were all above 88%. The reproducibility was high across all the replicate data. The average genotype concordance was 99.97%, and two key measurements, log intensity (*S*) and discrimination ratio, both had average correlations between replicates of greater than 0.97.

Please amend the paragraph beginning at line 26 of page 50 with the following amended paragraph:

WGSA DNA mixing experiments were performed as follows: the concentrations of genomic DNA from Hs-578T and Hs-578Bst were determined by PICOGREEN™ ~~PicoGreen~~ dsDNA Quantitation Assay (Molecular Probes) and Hs-578Bst DNA was added to Hs-578T DNA at10% increments.

Please amend the paragraph beginning at line 8 of page 81 with the following amended paragraph:

Methods of ~~identifying changes in~~ estimating genomic DNA copy number are disclosed. ~~Methods for identifying homozygous deletions and genetic amplifications are disclosed~~. Amplified genomic DNA is hybridized to an array of allele specific SNP probes to generate a hybridization pattern. A value, *S*, is calculated for individual SNPs in the experimental sample, where *S* is the log of the arithmetic average of the intensities of the perfect match probes for the SNP. *S* is calculated for the SNP in reference samples that are matched to the experimental sample in genotype. The mean and standard deviation for the S values of the reference samples are calculated and a log intensity difference is calculated by subtracting the mean values for the reference and experimental samples. The copy number of the SNP region is estimated using the difference between the mean for the SNP in the reference samples and the *S* value for the SNP in the experimental sample in a log-log linear model. ~~An array of probes designed to detect presence or absence of a plurality of different sequences is also disclosed. The probes are designed to hybridize to sequences that are predicted to be present in a reduced complexity sample. The methods may be used to detect copy number changes in cancerous tissue compared to normal tissue. The methods may be used to diagnose cancer and other diseases associated with chromosomal anomalies~~.